

ALIGNMENTS

RESULT 1

CXAR_MOUSE

ID CXAR_MOUSE STANDARD; PRT; 365 AA.

AC P97792; O09052;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).

GN CXADR OR CAR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RX MEDLINE=97190109; PubMed=9036860;

RA Bergelson J.M., Cunningham J.A., Drogue G., Kurt-Jones E.,

RA Krishivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;

RT "Isolation of a common receptor for Coxsackie B viruses and

RT adenoviruses 2 and 5.";

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C3H/MAI;

RX MEDLINE=97250541; PubMed=9096397;

RA Tomko R.P., Xu R., Philipson L.;

RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C

RT adenoviruses and group B coxsackieviruses.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RA Bergelson J.M., Krishivas A., Crowell T.L., Finberg R.W.;

RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B

RT viruses and adenoviruses.";

RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

CC -!!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Y10320; CAA71368.1; -.

DR EMBL; U90715; AAC53148.1; -.

DR EMBL; Y11929; CAA72679.1; -.

DR MGD; MGI:1201679; Cxadr.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003600; Ig_like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00410; IG_like; 1.

DR SMART; SM00408; IGc2; 1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR
 FT HOMOLOG.
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 340 365 VAAAPNLNSRMGVPMI PAQSKDGGSIV -> FKYAYKTDGI
 FT VV (IN REF. 2 AND 3).
 SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

RESULT 2
CXAR_HUMAN
ID CXAR_HUMAN STANDARD; PRT; 365 AA.
AC P78310; O00694;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-adenovirus receptor) (hCAR) (CVB3 binding protein).
GN CXADR OR CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E., Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20008750; PubMed=10543405;
RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A., Bowles N.E.;
RT "Genomic organization and chromosomal localization of the human Coxsackievirus B-adenovirus receptor gene.";
RL Hum. Genet. 105:354-359(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
RT "Sequence and expression of CXADR, the human gene for the coxsackievirus and adenovirus receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y07593; CAA68868.1; -.
DR EMBL; U90716; AAC51234.1; -.
DR EMBL; AF169366; AAF05908.1; -.
DR EMBL; AF169360; AAF05908.1; JOINED.

DR EMBL; AF169361; AAF05908.1; JOINED.
 DR EMBL; AF169362; AAF05908.1; JOINED.
 DR EMBL; AF169363; AAF05908.1; JOINED.
 DR EMBL; AF169364; AAF05908.1; JOINED.
 DR EMBL; AF169365; AAF05908.1; JOINED.
 DR EMBL; AF200465; AAF24344.1; -.
 DR MIM; 602621; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00408; IGc2; 1.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
 FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 41 120 BY SIMILARITY.
 FT DISULFID 162 212 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;

Query Match 17.0%; Score 343; DB 1; Length 365;
 Best Local Similarity 27.5%; Pred. No. 9e-16;
 Matches 106; Conservative 67; Mismatches 147; Indels 66; Gaps 14;

Qy	31	LQLHL PANRL QAVEGGEVVLPAWYTLHGEVSSSQPWEVPFVMWFFK--QKEKEDQVL SYI	88
	: : :: : : : : : : : : : : : : :		
Db	20	LSITT PEE MIE KAK GET AYL PCKFT LSP E --DQGPLDIE ---WLISPADNQKV DQVI ILY	74
Qy	89	NGVTT SKPGVSLVY-----SMP SRNL SLRLEG LQE KDS GP YSC VNV QD	132
	: : : : : : : : : : : : : : : : : :		
Db	75	SG-----DKIYDDYY PDLKGRV HFTSNDLKSGDASINV TNLQLSDIG TYQCKVK---	123
Qy	133	KQG KSR GH SIK TLE LNVL VLP APP SCRL QGV PH VGAN VTLS CQSPRS KPA VQY QWDR QLP	192
	: : : : : : : : : : : : : : : : : :		
Db	124	---KAPGVANKIHLVVLV KPSG ARCY VDG SEE IGSDF KIK CEP KEG SLP QYE WQKL SD	180
Qy	193	SFQT FFAP ALD VIR GS LS LT NL LSS MAG VY VCKAH NEV GTA QC NVT LE -VST GPG AAVVA	251
	: : : : : : : : : : : : : : : : : : :		
Db	181	SQKMPT SWLA EM TSS VIS VKN ASSE YSGT YS CT VRN RVG SDQ CL RL NVV PPS NKA GLIA	240
Qy	252	GAVV GTL VGL GLL AGL LVLL YHRRG KALE ---EPANDI KE DAIA PRT LPW PKSS DTISK N	307
	: : : : : : : : : : : : : : : : : : :		
Db	241	GAI IGT LLAL ALI -GLI IFCCR KK RREE KYE KEV HHD IRED -----VPPP KSRT STARS	293
Qy	308	GTL SS VTS SAR ALR RPPh --GPPR PG AL TPT PSL SS QAL P -SPRL PTT DG AHP QP I SPI PGG	364
	: : : : : : : : : : : : : : : : : : : :		
Db	294	YIGSNH SLSL GSMS PSNME GYS KT -QYN QVP SED FERT P QSP TL P -----PAK	339
Qy	365	VSS SGLS RMGA VP VM VP A QSQAG SLV	390
	: : : : : : : : : : : : : : : : : : :		
Db	340	VAAPN LSL RMGA IP VM IP A QSKD GS IV	365